

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/58,773  
Source: IFWP  
Date Processed by STIC: 6/14/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 06/14/2006

PATENT APPLICATION: US/10/581,773

TIME: 10:14:31

Input Set : A:\42100.txt

Output Set: N:\CRF4\06142006\J581773.raw

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4 <110> APPLICANT: Imperial College Innovations Limited
6 <120> TITLE OF INVENTION: Therapeutically Useful Molecules
8 <130> FILE REFERENCE: 28646/42100
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/581,773
C--> 11 <141> CURRENT FILING DATE: 2006-06-06
13 <150> PRIOR APPLICATION NUMBER: GB 0328363.7
14 <151> PRIOR FILING DATE: 2003-12-06
16 <160> NUMBER OF SEQ ID NOS: 18
18 <170> SOFTWARE: SeqWin99
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 9
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Peptide of WT1 which is presented by HLA-A2 class I molecules
28 <400> SEQUENCE: 1
29 Arg Met Phe Pro Asn Ala Pro Tyr Leu
30 1 5
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 6
34 <212> TYPE: PRT
35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: CDR1 of human TCR V -1.5 (V -8.2)
40 <400> SEQUENCE: 2
41 Ser Ser Tyr Ser Pro Ser
42 1 5
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 7
46 <212> TYPE: PRT
47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
50 <223> OTHER INFORMATION: CDR2 of human TCR V -1.5 (V -8.2)
52 <400> SEQUENCE: 3
53 Tyr Thr Ser Ala Ala Thr Leu
54 1 5
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 14
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: CDR3 of human TCR V -1.5 (V -8.2) - 1
64 <400> SEQUENCE: 4

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65 Val Val Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr
66 1          5          10
68 <210> SEQ ID NO: 5
69 <211> LENGTH: 12
70 <212> TYPE: PRT
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: CDR3 of human TCR V -175 (V -8.2) - 2
76 <400> SEQUENCE: 5
77 Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr
78 1          5          10
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 6
82 <212> TYPE: PRT
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: CDR1 of human TCR V -2.1 (V -20.1)
88 <400> SEQUENCE: 6
89 Asp Phe Gln Ala Thr Thr
90 1          5
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 7
94 <212> TYPE: PRT
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: CDR2 of human TCR V -2.1 (V -20.1)
100 <400> SEQUENCE: 7
101 Ser Asn Glu Gly Ser Lys Ala
102 1          5
104 <210> SEQ ID NO: 8
105 <211> LENGTH: 8
106 <212> TYPE: PRT
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: CDR3 of human TCR V -2.1 (V -20.1) - 1
112 <400> SEQUENCE: 8
113 Ser Ala Arg Asp Gly Gly Glu Gly
114 1          5
116 <210> SEQ ID NO: 9
117 <211> LENGTH: 11
118 <212> TYPE: PRT
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: CDR3 of human TCR V -2.1 (V -20.1) - 2
124 <400> SEQUENCE: 9
125 Arg Asp Gly Gly Glu Gly Ser Glu Thr Gln Tyr
126 1          5          10
128 <210> SEQ ID NO: 10
129 <211> LENGTH: 11

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130 <212> TYPE: PRT  
 131 <213> ORGANISM: Artificial Sequence  
 133 <220> FEATURE:  
 134 <223> OTHER INFORMATION: Framework amino acid sequence of constant portion C-terminal  
 to  
 135 CDR3  
 137 <400> SEQUENCE: 10  
 138 Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro  
 139 1 5 10  
 141 <210> SEQ ID NO: 11  
 142 <211> LENGTH: 5  
 143 <212> TYPE: PRT  
 144 <213> ORGANISM: Artificial Sequence  
 146 <220> FEATURE:  
 147 <223> OTHER INFORMATION: Beginning of constant region of human TCR V -1.5 (V -8.2)  
 149 <400> SEQUENCE: 11  
 150 Tyr Ile Gln Asn Pro  
 151 1 5  
 153 <210> SEQ ID NO: 12  
 154 <211> LENGTH: 5  
 155 <212> TYPE: PRT  
 156 <213> ORGANISM: Artificial Sequence  
 158 <220> FEATURE:  
 159 <223> OTHER INFORMATION: Beginning of framework amino acid sequence of human TCR V -  
 2.1 (V  
 160 -20.1)  
 162 <400> SEQUENCE: 12  
 163 Ser Glu Thr Gln Tyr  
 164 1 5  
 166 <210> SEQ ID NO: 13  
 167 <211> LENGTH: 10  
 168 <212> TYPE: PRT  
 169 <213> ORGANISM: Artificial Sequence  
 171 <220> FEATURE:  
 172 <223> OTHER INFORMATION: Part of framework amino acid sequence of human TCR V -2.1 (V  
 -20.1)  
 174 <400> SEQUENCE: 13  
 175 Phe Gly Pro Gly Thr Arg Leu Leu Val Leu  
 176 1 5 10  
 178 <210> SEQ ID NO: 14  
 179 <211> LENGTH: 5  
 180 <212> TYPE: PRT  
 181 <213> ORGANISM: Artificial Sequence  
 183 <220> FEATURE:  
 184 <223> OTHER INFORMATION: Part of constant region of human TCR V -2.1 (V -20.1)  
 186 <400> SEQUENCE: 14  
 187 Glu Asp Leu Lys Asn  
 188 1 5  
 190 <210> SEQ ID NO: 15  
 191 <211> LENGTH: 830  
 192 <212> TYPE: DNA  
 193 <213> ORGANISM: Human TCR V -1.5 (V -8.2)

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195 &lt;400&gt; SEQUENCE: 15

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196 atgctcctgc tgctcgtccc agtgctcgag gtgattttta ctctgggagg aaccagagcc 60
197 cagtcggtga cccagcttga cagccacgtc tctgtctctg aaggaacccc ggtgctgctg 120
198 aggtgcaact actcatcttc ttattcacca tctctcttct ggtatgtgca acaccccaac 180
199 aaaggactcc agcttctcct gaagtacaca tcagcggcca ccttggttaa aggcatacaac 240
200 ggttttgagg ctgaatttaa gaagagtgaac acctccttcc acctgacgaa accctcagcc 300
201 catatgagcg acgcggctga gtacttctgt gttgtgagtc ctttttcagg aggaggtgct 360
202 gacggactca cctttggcaa agggactcat ctaatcatcc agccctatat ccagaacctt 420
203 gacctgccc tgtagcagct gagagactct aaatccagtg acaagtctgt ctgcctattc 480
204 accgattttg attctcaaac aaatgtgtca caaagtaagg attctgatgt gtatatcaca 540
205 gacaaaactg tgctagacat gaggtctatg gacttcaaga gcaacagtgc tgtggcctgg 600
206 agcaacaaat ctgactttgc atgtgcaaac gccttcaaca acagcattat tccagaagac 660
207 accttcttcc ccagcccaga aagttcctgt gatgtcaagc tggtcgagaa aagctttgaa 720
208 acagatacga acctaaactt tcaaaacctg tcagtgattg gggtccgaat cctcctcctg 780
209 aaagtggccg ggtttaatct gctcatgacg ctgcggctgt ggtccagctg 830

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211 &lt;210&gt; SEQ ID NO: 16

212 &lt;211&gt; LENGTH: 276

213 &lt;212&gt; TYPE: PRT

214 <213> ORGANISM: Human TCR V<sub>α</sub>-1.5 (V -8.2)

216 &lt;400&gt; SEQUENCE: 16

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217 Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly
218 1 5 10 15
220 Gly Thr Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val
221 20 25 30
223 Ser Glu Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr
224 35 40 45
226 Ser Pro Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln
227 50 55 60
229 Leu Leu Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn
230 65 70 75 80
232 Gly Phe Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr
233 85 90 95
235 Lys Pro Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val
236 100 105 110
238 Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly
239 115 120 125
241 Thr His Leu Ile Ile Gln Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val
242 130 135 140
244 Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
245 145 150 155 160
247 Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
248 165 170 175
250 Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
251 180 185 190
253 Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
254 195 200 205
256 Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
257 210 215 220
259 Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu

```

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260 225          230          235          240
262 Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
263          245          250          255
265 Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
266          260          265          270
268 Leu Trp Ser Ser
269          275
271 <210> SEQ ID NO: 17
272 <211> LENGTH: 933
273 <212> TYPE: DNA
274 <213> ORGANISM: Human TCR V -2.1 (V -20.1)
276 <400> SEQUENCE: 17
277 atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa 60
278 catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccttg 120
279 gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg 180
280 atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgctga gaaggacaag 240
281 tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccactct 300
282 gaagacagca gcttctacat ctgcagtgtc agagatgggg gggagggttc ggagaccag 360
283 tcttcgggc caggcacgcs gctcctggtg ctcgaggacc tgaaaaagct gttccacccc 420
284 gaggtcgctg tgtttgagcc atcagaagca gagatctccc acacccaaaa ggccacactg 480
285 gtgtgcctgg ccacaggctt ctaccccgac cagctggagc tgagctggtg ggtgaatggg 540
286 aaggaggtgc acagtggggc cagcacagac ccgcagcccc tcaaggagca gcccgccttc 600
287 aatgactcca gatactgcct gagcagccgc ctgaggggtct cggccacctt ctggcagaac 660
288 ccccgcaacc acttccgctg tcaagtccag ttctacgggc tctcggagaa tgacgagtgg 720
289 acccaggata gggccaaacc tgtcaccagc atcgtcagcg ccgaggcctg gggtagagca 780
290 gactgtggct tcacctccga gtcttaccag caaggggtcc tgtctgccac catcctctat 840
291 gagatcttgc tagggaaggc caccttgtat gccgtgctgg tcagtgcctc cgtgctgatg 900
292 gccatggtca agagaaagga ttccagaggc tag 933
294 <210> SEQ ID NO: 18
295 <211> LENGTH: 310
296 <212> TYPE: PRT
297 <213> ORGANISM: Human TCR V -2.1 (V -20.1)
299 <400> SEQUENCE: 18
300 Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
301 1          5          10          15
303 Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
304          20          25          30
306 Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
307          35          40          45
309 Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
310          50          55          60
312 Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
313 65          70          75          80
315 Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
316          85          90          95
318 Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Asp
319          100          105          110
321 Gly Gly Glu Gly Ser Glu Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu
322          115          120          125

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VERIFICATION SUMMARY

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TIME: 10:14:32

Input Set : A:\42100.txt

Output Set: N:\CRF4\06142006\J581773.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date